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RAW SEQUENCE LISTING

DATE: 02/01/2002

PATENT APPLICATION: US/09/966,881

TIME: 11:36:29

Input Set : N:\Crf3\RULE60\09966881.raw

Output Set: N:\CRF3\02012002\I966881.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Seymour, Graham

3 Bird, Colin

4 Medina-Suarez, Rosybel

5 (ii) TITLE OF INVENTION: Genetic control Of Fruit Ripening

6 (iii) NUMBER OF SEQUENCES: 57

7 (iv) CORRESPONDENCE ADDRESS:

8 (A) ADDRESSEE: Zeneca Ag Products Inc.

9 (B) STREET: 1800 Concord Pike

10 (C) CITY: Wilmington

11 (D) STATE: DE

12 (E) COUNTRY: USA

13 (F) ZIP: 19850

14 (v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Floppy disk

16 (B) COMPUTER: IBM PC compatible

17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

18 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

19 (vi) CURRENT APPLICATION DATA:

C--> 20 (A) APPLICATION NUMBER: US/09/966,881

C--> 21 (B) FILING DATE: 28-Sep-2001

22 (C) CLASSIFICATION:

23 (vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: US/09/242,860

26 (B) FILING DATE: 29-Mar-1999

27 (A) APPLICATION NUMBER: GB 9618862.8

28 (B) FILING DATE: 10-SEP-1996

29 (A) APPLICATION NUMBER: GB 9708366.1

30 (B) FILING DATE: 25-APR-1997

31 (A) APPLICATION NUMBER: PCT/GB97/02424

32 (B) FILING DATE: 08-SEP-1997

33 (viii) ATTORNEY/AGENT INFORMATION:

34 (A) NAME: Hohenschutz, Liza D.

35 (B) REGISTRATION NUMBER: 33,712

36 (C) REFERENCE/DOCKET NUMBER: SEE 50183/UST

37 (ix) TELECOMMUNICATION INFORMATION:

38 (A) TELEPHONE: (302) 886-1699

39 (2) INFORMATION FOR SEQ ID NO: 1:

40 (i) SEQUENCE CHARACTERISTICS:

41 (A) LENGTH: 785 base pairs

42 (B) TYPE: nucleic acid

43 (C) STRANDEDNESS: single

ENTERED

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44      (D) TOPOLOGY: unknown
45      (ii) MOLECULE TYPE: cDNA
46      (vii) IMMEDIATE SOURCE:
47          (B) CLONE: U-U9
48      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
49      CCGCACGAGG AAAAAGTANG TGAGAANGAG ATAATCGTTG ACCGAGGNAG AGAATGGCGA      60
50      GCGAGAAGAG CAAAATCCTG ATCATCGGGG GCACCGGGTA CATCGGCAAG TTCATCGTGT      120
51      TTGCGAGCGC CAGGTTAGGT AACCTACCT TCGCTCTCGT CCGGAGCACC ACCGCCCCCG      180
52      CCGCCAACC CGAGAAGGCC AAGCTCCTGA GCGACTTCCA GGCCGCCGGC GTCACCCTCG      240
53      TCCAGGGGGA TATNTATAAC CACGAGAGTC TGGTTAAGGC GATCAAGCTG GTGGATGTGG      300
54      TCATCTCCCC CGTCGGCTTC GGGCANCTGA NTGATCAGAC CAAGATCATC GACGCCATCN      360
55      AANAAGCCGG AGGACACATC AAGAGGTACC TTCCATCGGA GTTTGGCAAC GACGTANACC      420
56      GAAGCCATGC TGTGGAGCCA GCAAAGTCTA CCTTTGTCGT CAAGCAACAA ATCANAAGGG      480
57      CTGTTGAGGC ATCGGGTNTC CCTTACACCT TTGTATCTTC CAACTTTCTT CGGTGGGTNT      540
58      TTCCTCCCGG TATTATGACA GGCAGGAGCC ACTGGTCCTC CCACGGACAA GGTGTGCATC      600
59      TTAGGTNACG GGAACNCAA ACGATCTTCT CNATGAANAC GACTTCCGGA CATCCCATTT      660
60      ANTCTTGAT GATCCATAAC CTGAACCAGG TTCTATTTCT TAAAACTTCC NCCACTTCTT      720
61      NTCTCTTANC ANCTCNTTTC CCTCTTGGGA AAAAAATGTC NNCTANACTT CNAAGGGT      780
62      TTANT      785
64 (2) INFORMATION FOR SEQ ID NO: 2:
65      (i) SEQUENCE CHARACTERISTICS:
66          (A) LENGTH: 813 base pairs
67          (B) TYPE: nucleic acid
68          (C) STRANDEDNESS: single
69          (D) TOPOLOGY: unknown
70      (ii) MOLECULE TYPE: cDNA
71      (vii) IMMEDIATE SOURCE:
72          (B) CLONE: U-U17
73      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
74      CGCGCACGAG GAAGAAAAGT AGGTGAGAAN GAGATAATCG TTGACCGAGG NAGAGAATGG      60
75      CGAGCGAGAA GAGCAAAATC CTGATCATCG GGGGCACCGG GTACATCGGC AAGTTCATCG      120
76      TGTTTGCAGG CGCCAGGTTA GGTAACCCTA CCTTCGCTCT CGTCCGGAGC ACCACCGCCC      180
77      CCGCCGGCCA ACCCGAGAAG GCCAAGCTCC TGAGCGACTT CCAGGCCGCC GCGGTCACCC      240
78      TCGTCCAGGG GGATATATAT AACCACGAGA GTCTGGTTAA GGCGATCAAG CTGGTGATG      300
79      TGGTCATCTC CCGGTCGGC TTCGGGCANC TGANTGATCA GACCAAGATC ATCGACGCCA      360
80      TCAAAGAAGC CGGAGGACAC ATCAAGAGGT ACCTTCCATC GGAGTTTGGC AACGACGTAN      420
81      ACCGAAGCCA TGCTGTGGAG CCAGCAAAGT CGACCTTTGT CGTCAAGCAA CAAATCANAA      480
82      GGGCTGTTGA GGCATCGGGT ATCCCTTACA CCTTTGTATC TTCCAATTC TTCGGTGGGT      540
83      NTTTTCTCCC GGTATTANGA CAGGCAGGAG CCACTGGTCC TCCACGGAC AAGGTTGTCA      600
84      TCTTANGTGA CGGGAACACA AAAGCGATCT TTCTCAATGA ANACACATCC GGACNTNCAC      660
85      NATTAAGCA GTGGATGATC CGAAAACCTG AACANGTTCT ATATCTGAAA CCTCCGCCA      720
86      CTCTTGCTC ATNACAATC ATTTCCCTCT GGGAAAAAAA NGTCNGCAA ACTCCNAAAA      780
87      GGTCTACTTC CCGGAAGAAA AATCTGAANC ANA      813
89 (2) INFORMATION FOR SEQ ID NO: 3:
90      (i) SEQUENCE CHARACTERISTICS:
91          (A) LENGTH: 746 base pairs
92          (B) TYPE: nucleic acid
93          (C) STRANDEDNESS: single
94          (D) TOPOLOGY: unknown

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95      (ii) MOLECULE TYPE: cDNA
96      (vii) IMMEDIATE SOURCE:
97          (B) CLONE: U-U66
98      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
99      GGCACGAGGG GAAAAGGAGA TNATCGTTGA CCGAGGAGAG AATGGCGAGC GAGAAGAGCA      60
100     AGATCCTGAT CATCGGGGGC ACGGGGTACA TCGGCAAGTT CATCGTGTTC GCGAGCGCCA      120
101     GGTTAGGTAA CCCTACCTTC GCTCTCGTCC GGAGCACCAC CGCCCCCGCC GGCCAACCCG      180
102     AGAAGGGCAA GCTCCTGAGC GACTTCCAGG CCGCCGCGCT CACCCTGGTC CAGGGGGATA      240
103     TATATAACCA CNAGAGTCTG GTTAAGGCGA TCAAGCTGGT GGATGTGGTC ATCTCCCCCG      300
104     TCGGCTTCGG GCAGCTGAGT GATCAGACTA AGATCATCGA CGCCATCAAA GAAAGCCGGA      360
105     GGACACATCA AGAGGTACCT TCCATCGGGA GTTTGGCAAC GACGTANACC GAAGCCATGC      420
106     TGTGGAAGCC ANCAAAGTCG ACCTTTGTCT TCAAGCAACA AATTANAAGG GCTGTTGAGG      480
107     CATCGGGGAT CCCTTACACC TTTGTTATCT TCCAATTCT TCGGTGGGTA TNTCCTCCCC      540
108     GTATTGGGAC AGGCANGAAC CACTGGTCCT CCCCACGGAC AAGGTTGTCN TCTTAGGTGA      600
109     ACGGGAACAC CAANGCGATC TTTCTCAATG AAAGACAAC TCGGACATNC CCNATTTAAC      660
110     CANTGGATGA TCCNANAACC TGAACAAGT CTATTCTGA AAAC TTCNCC ATCTTCTTTT      720
111     TCTCATAACG AACCCNTTTN CCTCTT      746
113 (2) INFORMATION FOR SEQ ID NO: 4:
114     (i) SEQUENCE CHARACTERISTICS:
115         (A) LENGTH: 795 base pairs
116         (B) TYPE: nucleic acid
117         (C) STRANDEDNESS: single
118         (D) TOPOLOGY: unknown
119     (ii) MOLECULE TYPE: cDNA
120     (vii) IMMEDIATE SOURCE:
121         (B) CLONE: U-U104
122     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
123     GGCACGAGGA AANGAGATAA TCGTTGACCG AGGCAGAGAA TGGCGAGCGA GAAGAGCAAA      60
124     ATCCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTTTGC GAGCGCCAGG      120
125     TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCACCG CCCCCGCCGG CCAACCCGAG      180
126     AAGGCCAAGC TCCTGAGCGA CTTCCAGGCC GCCGCGTCA CCCTCGTCCA GGGGGATATA      240
127     TATAACCACG AGAGTCTGGT TAAGGCGATG AAGCTGGTGG ATGTGGTCAT CTCCCCCGTC      300
128     GGCTTCGGGC AGCTGAGTGA TCAGACCAAG ATCATCGACG CCATCAAAGA AGCCGGAGGA      360
129     CACATCAAGA GGTACCTTCC ATCGGGAGTT TGGCAACGAC GTTANACCGA AGCCATGCTG      420
130     TGGAGCCAGC AAAGTCNACC TTTGTCGTCA AGCAACAAAT CANAAGGGCT GTTGANGCAT      480
131     CGGGTNTCCC TTACACCTTT GTATCTTCCA ACTTCTTCGG TGGGTATTTC CTCCCGGTAT      540
132     TANGACAGGC AGGACCACTG GTCCTCCCEA CNGACAAGGT TGTCTCTTA GGTGACNGGA      600
133     ACACAAAANC ATCTTTCTCN ATGAAGACAA CTCCGGACAT ACNCNATTAA AGCNGTGGAT      660
134     GATCCCAAAA CCTGAACAAG TTCCTATNTC TTGAAAACCT TCCCGCCCAA CCATCCTTTN      720
135     GTTCTCCCNT TAAACCNAAC CTCCATTTTC CCCTCCTTGG GGAAAAAAA AAGGTCCGGC      780
136     NAANAAC TTC CNA      795
138 (2) INFORMATION FOR SEQ ID NO: 5:
139     (i) SEQUENCE CHARACTERISTICS:
140         (A) LENGTH: 797 base pairs
141         (B) TYPE: nucleic acid
142         (C) STRANDEDNESS: single
143         (D) TOPOLOGY: unknown
144     (ii) MOLECULE TYPE: cDNA
145     (vii) IMMEDIATE SOURCE:

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146      (B) CLONE: U-U13
147      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
148      CGGCACGAGG NAGAACCTTT TGACAGAGTT GTTGTCATGG CAACAAAAGC TTCTCTCTCC      60
149      ATAAAAGGCT TTGCCTTGCT GGTTCAGTC CTTGTAGCAG TTCCAACAAG AGTGCAATCG      120
150      ATTGGTGTCT GCTACGGCAT GCTCGGCAAC AATCTTCCCC CGCCCAGCGA GGTGGTCAGT      180
151      CTCTACAAAT CCAACAACAT CGCGAGGATG AGACTCTACG ATCCAAACCA AGCCGCCCTG      240
152      CAAGCCCTCA GGAACTCCAA CATCCAAGTC CTGTTGGATG TCCCCGATC CGACGTGCAG      300
153      TCACTGGCCT CCAATCCTTC GGCCGCCGGC GACTGGATCC GGAGGAACGT CGTCGCCTAC      360
154      TGGCCAGCG TCTCCTTTTCG ATACATAGCT GTCGGAAACG AGCTGATCCC CGGATCGGAT      420
155      CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC      480
156      CTGCAAAACC AGATCAAGGT CTCGACCGCG GTCGACACGG GCGTCCTCGG CACGTCCTAC      540
157      CCTCCCTCCG CCGGCGCCTT CTCCTCCGCC GCCCAGGCGT TACCTGANCC CCATCGTGCA      600
158      GTTCTTGGCG ANTAACGGAA CGCCGCTCCT GGTCAATGTG TACCTTATTT TAACTACACC      660
159      GGCAACCCGG GANAGATCTC GCTGCCTACN CCCTGTTTAC GGCCNCGGGG TCTCNTGCAG      720
160      GATGGGCGAA TTCCNCTATC ANAANCTGTT CANTCCATCT TCNAAACCGG TCTTCCCGGG      780
161      CTGGAAAAAA TTGAAG      797
163      (2) INFORMATION FOR SEQ ID NO: 6:
164      (i) SEQUENCE CHARACTERISTICS:
165          (A) LENGTH: 792 base pairs
166          (B) TYPE: nucleic acid
167          (C) STRANDEDNESS: single
168          (D) TOPOLOGY: unknown
169      (ii) MOLECULE TYPE: cDNA
170      (vii) IMMEDIATE SOURCE:
171          (B) CLONE: U-U136
172      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
173      GGCACGAGGA GAACCCTTTT GACAGAGTTG TTGTCATGGC AACAAAAGCT TCTCTCTCCA      60
174      TAAAAGGCTT TGCCTTGCTG GTTTCAGTCC TTGTAGCAGT TCCAACAAGA GTGCAATCGA      120
175      TTGGTGTCTG CTACGGAATG CTCGGCAACA ATCTTCCCCC GCCCAGCGAG GTGGTCAGTC      180
176      TCTACAAATC CAACAACATC GCGAGGATGA GACTCTACGA TCCAAACCAG GCCGCCCTGC      240
177      AAGCCCTCAG GAATCCCAAC ATCCAAGTCC TGTGGATGT CCCCCGATCC GACGTGCAGT      300
178      CACTGGCCTC CAATCCTTCG CCGGCCGGCG ACTGGATCCG GAGGGAACGT CGTCGCCTAC      360
179      TGGCCACGCG TCTCCTTTTCG ATACATAGCT GTCGGAAACG ANCTGATCCC CGGATCGGAT      420
180      CTGGCGCAGT ACATCCTCCC CGCCATGCGC AACATCTACA ATGCTTTGTC CTCGGCTGGC      480
181      CTGCAAAACC AGATCAAGGT CTCCGACCGC GGTGACACG GGCGTCCTCG GCACGTCCTA      540
182      CCTCCCTCC CGCCGGNGCG TTCTCCTCCG CCGCCCAAGC GTNCTGANCC CCATCGTGCA      600
183      NTTCTTTGGC GAAATAACGG ANCGCCGCTC CCNGGTCCAT GTTTTTCCTT TATTTTAACT      660
184      ACNCCGGCAA CCCNGGAAAG ATTTGCTGCG CTTACGCCC CCTGGTTTCC NNGGGGCTTC      720
185      CCGGGCGTTT CTTCTTTTGC CAGGGANTNG GGGCGAATC CCNNCTTTTC CANAAACCTT      780
186      GTTCCAACNC CC      792
188      (2) INFORMATION FOR SEQ ID NO: 7:
189      (i) SEQUENCE CHARACTERISTICS:
190          (A) LENGTH: 855 base pairs
191          (B) TYPE: nucleic acid
192          (C) STRANDEDNESS: single
193          (D) TOPOLOGY: unknown
194      (ii) MOLECULE TYPE: cDNA
195      (vii) IMMEDIATE SOURCE:
196          (B) CLONE: U-U21

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197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
198 CGGCACGAGT CTCTCTCTGT CTCTCCGTCG TCTCGTTGTC TGTTTCGTTAG GGCTTGCGAT 60
199 CGCCACCGGT CGCGAGGGTT GGAGCCATGG AATTCTTGCG GTTTGGGGCT GAGGTGGCGG 120
200 CAGGAGAGGA AGCCGCGACG GGGTACTGGA TGCATGGCA GACGCTCGTC TGCCTCTGA 180
201 TCGTCGTCGC CCCGGCGGTC GCCGCGGTGG TTGTCGCGGC GCGGGCGCCG GCGCCGGCGC 240
202 GACCGCTCAG GGCCGTCGAT CTCTGGGCGC CGTGCTGGGC CGGGATGCAC CCGGCCCTGGC 300
203 TTCTCGCGTA CCGCGGCTTC NTGTTCTTGG CCATGGCGTG GCTACTCTTC CANATGATTC 360
204 TGTTTCGCGG ATTCTCCGCG TTCTACTTCT ATACTCAGTG GACGTTTGCC TTAGTCATTG 420
205 TCTATTTTGC GATCGCAACC ATTATATCCG CCCATGGCTG CTGGCTTTAC TCAAAGAGAA 480
206 GTATTATGCC AGATCAGGAG GTCAACAGAT TCCTAAATGG TGGTTTGTAG CANAATAGTC 540
207 CTATGACTCT ACCTTTGAGG ACCAACAAAA ATATGAATGT TATAAGATTG CAAAGCTATC 600
208 NTGAACAGGA NGCTGATGAA NAAAAANCTG GATTTTGGGG TCCTGCTATG CNACTNGTCT 660
209 ATCAAAACCA TTGCANGTGC TGTAATTGTT GAAANACATT GTATTTTGGG NTCNTNCTAA 720
210 TACCATATTT GTCTTCTATA AATTTTCAGGC TAAATGCTAT AATGGGCTGC ATGCATTCTC 780
211 TTAATGCTGT GTTCTTCNA ATCCAACACT TTTCTCAATA ACCTGCCATT CCCNTNTTTC 840
212 NAATGGCATT TTTGC 855

214 (2) INFORMATION FOR SEQ ID NO: 8:
215 (i) SEQUENCE CHARACTERISTICS:
216 (A) LENGTH: 722 base pairs
217 (B) TYPE: nucleic acid
218 (C) STRANDEDNESS: single
219 (D) TOPOLOGY: unknown
220 (ii) MOLECULE TYPE: cDNA
221 (vii) IMMEDIATE SOURCE:
222 (B) CLONE: U-U31

223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
224 CGGCACGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA GAGAGAGAGA 60
225 GAGAGAGAGC CTAGACCGGC ATCNTCGTGC TTGCCGAGGG GCGGCTTATG ANTCTTGGTT 120
226 GTGCCACTGG GCATCCCAGC TTCGTCNTGT CCTGCTCCTT CACCANCCAN GTGATNGCAC 180
227 NACTGGANTT ATGGANGGAA ANGGCGACCG GCNNGTACGA NAAGAANGTC TATGTGCTGC 240
228 CCANGCNTCT GGATGAGAGG GTGGCNGCGC TCCNCCTCGG CAAGCTGGGT GCCNCGCTCA 300
229 CCNAGCTTAC NCCNTCGCGG GCTGATTACA TTAGCGTCCC GATCGAGGGA CCCTACANGC 360
230 CTGCTCACTA CNGGTATTNG GGTGCTTNTT GCNAGAGACG ATGATNATAN NTCGGAGCAC 420
231 TGGCNTTTTC GACTANNAGT TTGACCGATG GCTATGTTCG TTTTGCTTTT CACCTTTTGT 480
232 CTTCCCATCT TTGCTGGTTC ACCTATGGAC GTTTGTTCCTA TTTGGATGTN NTGAGAAATG 540
233 CTGATGGCAT TTTCGGAAAN AAAAAANATNT AAAATCNCGA GAGTTCTTCT ANAGCGGCCG 600
234 CGGGCCCNTC NNTTTTCCCC CGGGTGGGGT ACCANGTTTG TTGTNCCCNT TCCCCCTNTT 660
235 TGAGTCCTTT TACTNCCCCT GGCCGTCGTT TTATACNTCG TTGACTGGGA ANACCCTGCC 720
236 NT 722

238 (2) INFORMATION FOR SEQ ID NO: 9:
239 (i) SEQUENCE CHARACTERISTICS:
240 (A) LENGTH: 793 base pairs
241 (B) TYPE: nucleic acid
242 (C) STRANDEDNESS: single
243 (D) TOPOLOGY: unknown
244 (ii) MOLECULE TYPE: cDNA
245 (vii) IMMEDIATE SOURCE:
246 (B) CLONE: U-U131
247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]